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CTCGGGTACAACACTGACAATAAAGAGTACGTTCTTGTTAACTTA
AGGGTTTTTCTTCTGAAGATAAAGGCGAGTGGAACTGAACTCGA
TAATGCGGGTAAC GGTCAAGCAGTAATTCGTTTTCTTCGTCTAAA
AATGATGAACAAGCACCATTTCGAATTCTTGTAATCACGGTTTCA
AGAAAAATGGTAAATGGTATATTGAAACATCATCTACCCATGATT
ACGATTCTCCAGTACAATACATCAGTAAAAATGATCTCGGG

(SEQ ID NO:1)

FIG.1

CCATGGGTTTTTCTTCTGAAGATAAAGGCGAGTGGAACTGAACT
CGATAATGCGGGTAACGGTCAAGCAGTAATTCGTTTTCTTCGTCTA
AAAATGATGAACA AGCACCATTTCGAATTCTTGTAATCACGGTTTC
AAGAAAAATGCTAAATGGTATATTGAAACATCATCTACCCATGATT
ACGATTCTCCAGTACAATACATCAGTAAAAATGATCTCGGGTACAAC
ACTGACAATAAACACCACCACCACCACCAC

(SEQ ID NO:2)

FIG.2

CATATGAGCGATAAAATTATTCACCTGACTGACGACAGTTTTGACAC
GGATGTACTCAAAGCGGACGGGGCGATCCTCGTCGATTTCTAGAGTG
GTGCGGTCCGTGCAAAATGATCGCCCCGATTCTGGATGAAATCGCT
GACGAATATCAGGGCAAACGACCGTTGCAAACTGAACATCGATC
AAAACCCTGCTCACTGCGCCGAAATATGGCATCCGTGGTATCCCG
ACTCTGCTGCTGTTCAAAAACGGTGAACACCACCACCACCACCAC

(SEQ ID NO:5)

FIG.3

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CCATGCTCATATGAGCGATAAAATTATTACCTGACTGACGACAGTT
TTGACACGGATGTACTCAAAGCGGACGGGGCGATCCTCGTCGATTTC
TGGGCAGAGTGGTGCGGTCCGTGCAAATGATCGCCCCGATTCTGGA
TGAAATCGCTGACGAATA TCAGGGCAAACCTGACCGTTGCAAACCTG
AACATCGATCAAACCCTGGCACTG CGCCGAAATATGGCATCCGTGGT
GGACTCGGGTACAACACTGACAATAAACACCACCACCACCACCAC

(SEQ ID NO:8)

FIG.4

CTCGGGAGCGATAAAATTATTACCTGACTGACGACAGTTTTGACA
CGGATGTACTCAAAGCGGACGGGGCGATCCTCGTCGATTTCTGGGC
AGAGTGGTGCGGTCCGTGCAAATGATCGCCCCGATTCTGGATGAA
ATCGCTGACGAATATCAGGG CAAACTGACCGTTGCAAACCTGAAC
ATCGATCAAACCCTGGCACTGCGCCGAAATATGGCATCCGTGGTA
TCCCGACTCTGCTGCTGTTCAAAAACGGTGAAGTGGCGGCAACCAA
ACTCGGG

(SEQ ID NO:11)

FIG.5

CTCGGGAAGCTGACTAATCCGGAAGTAGAACTGCCGAACGCAGAAC
TGCTAGGCAAACGCCGTCTGGAAAAATTCGCCGCTAAAGTACAGCA
GCAGCTGGAAAGCAGCGATCTGGATCAATACCGCGCACTGCTCGGG

(SEQ ID NO:14)

FIG.6

CTCGGGGCACATAAAATGCTAAAAGATACAGGCATTATTGCTATCA
GCATTGATGACTATGAATTTGCTCATTTAAAAATACTGATGGATAA
AATTTTCGGTGAAGATAATTTATCGGAAATATCGTCGTTTGTCGT
TCAAAAAATGGAAAAGTGAGC AAGCGAAATATAGCGTCTGCTCAT
GAATATTTACTGGTTTATGGAAAATCAGATATGGCGGAACTATCTG
GACAACCAGATGATAAATCTCTTTATGATAAAGTTGATTGTTTTGG
TGAATATAGAATTGACGGAATGTTTCAGAAAAAAGGTGATTCAAG
TTTGAGAACTGATCGCCCTAATATGTTTTATCCTTTATATTTAACC
CATCAACAGGTGAAGTACAGGTAGAGCCAGAACTCGGG

(SEQ ID NO:17)

FIG.7

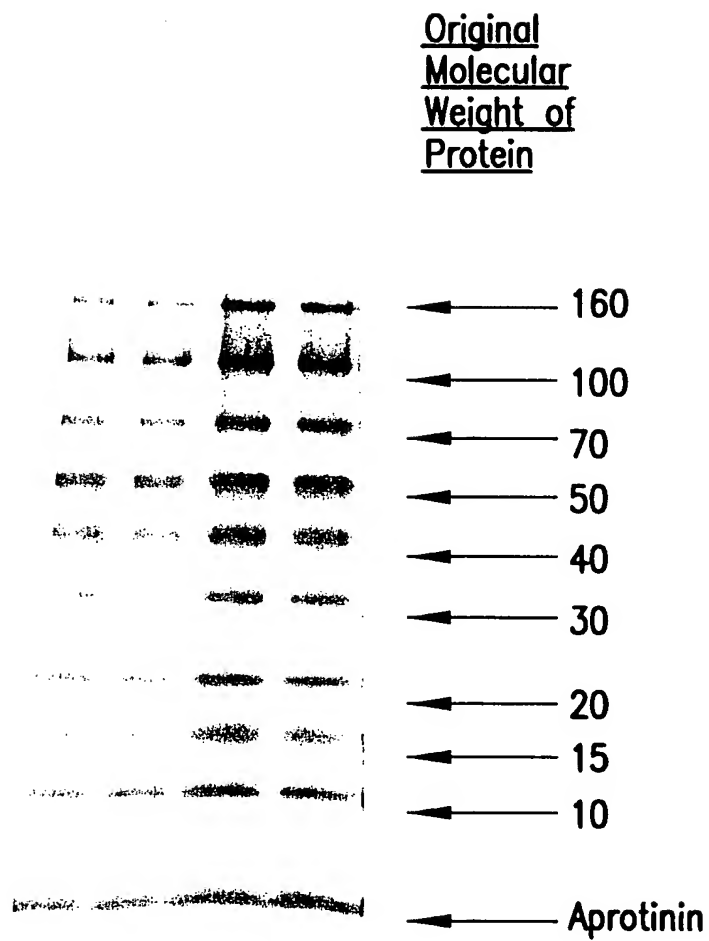


FIG.8

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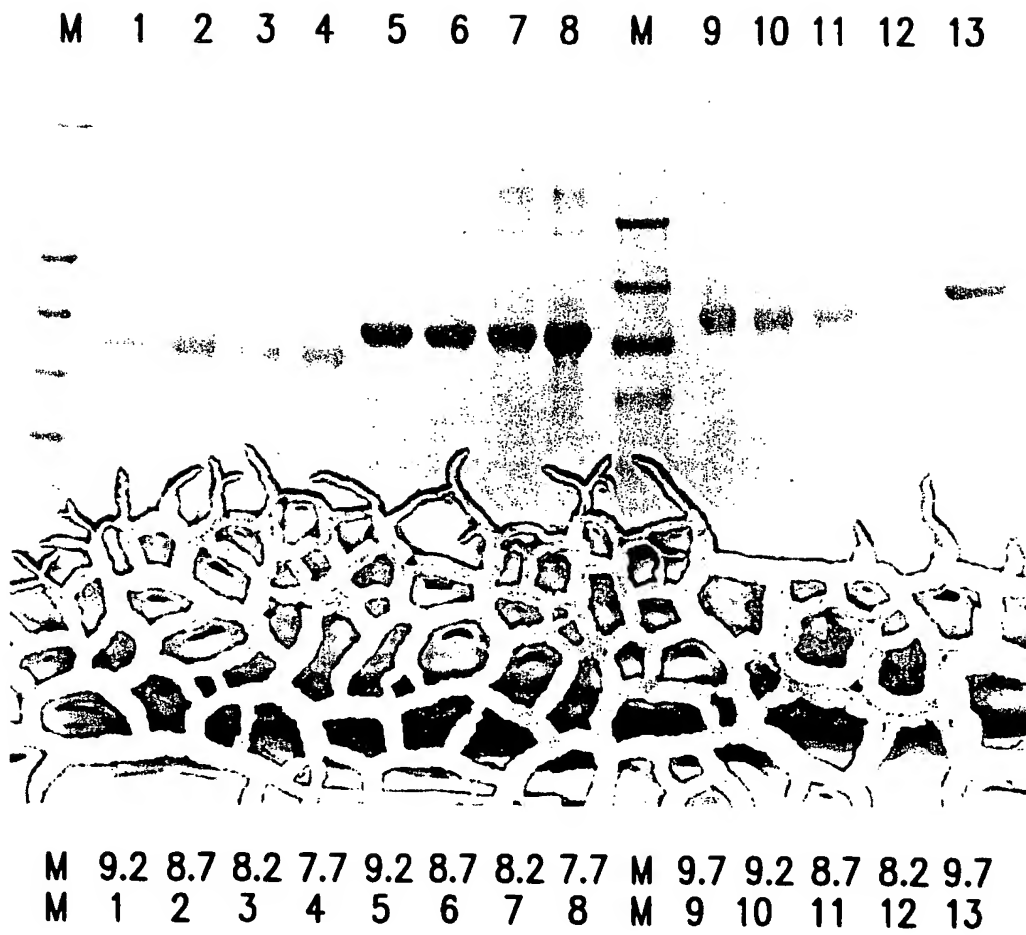


FIG.9

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1 2 3 4 5 6 M 7 8 9 10 11 12 13 14



pH: 7.2 8.2 9.2 7.2 8.2 9.2 M 7.2 8.2 9.2 7.2 8.2 9.2 9.2 8.7
Lane: 1 2 3 4 5 6 M 7 8 9 10 11 12 13 14

FIG.10

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1 2 3 M 4 5 6 7 8 9 10 11 12 13 14



pH:	7.2	8.2	9.2	M	7.2	8.2	9.2	7.2	8.2	9.2	7.2	8.2	9.2	8.2	9.7
Lane:	1	2	3	M	4	5	6	7	8	9	10	11	12	13	14

FIG.11

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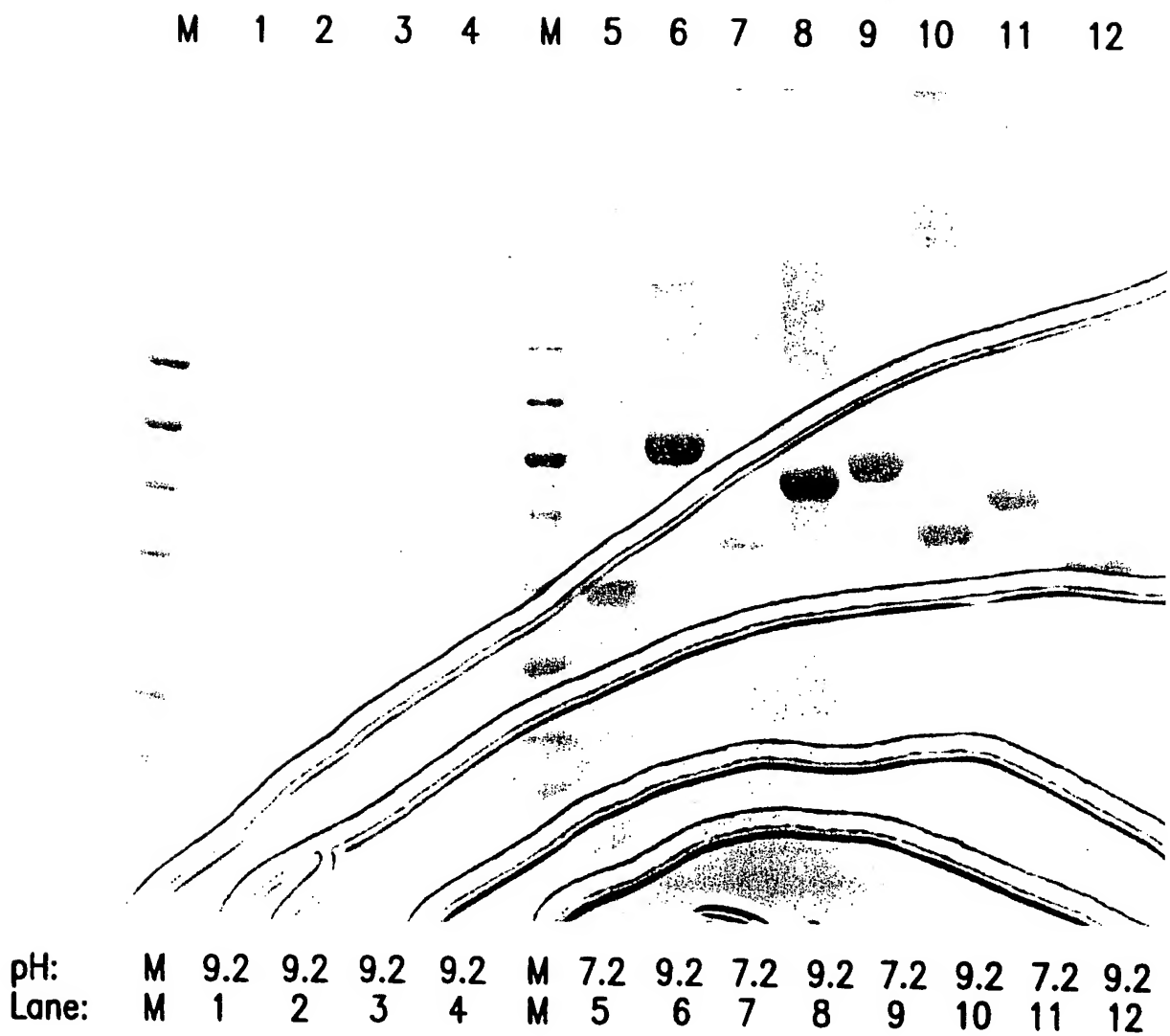


FIG.12

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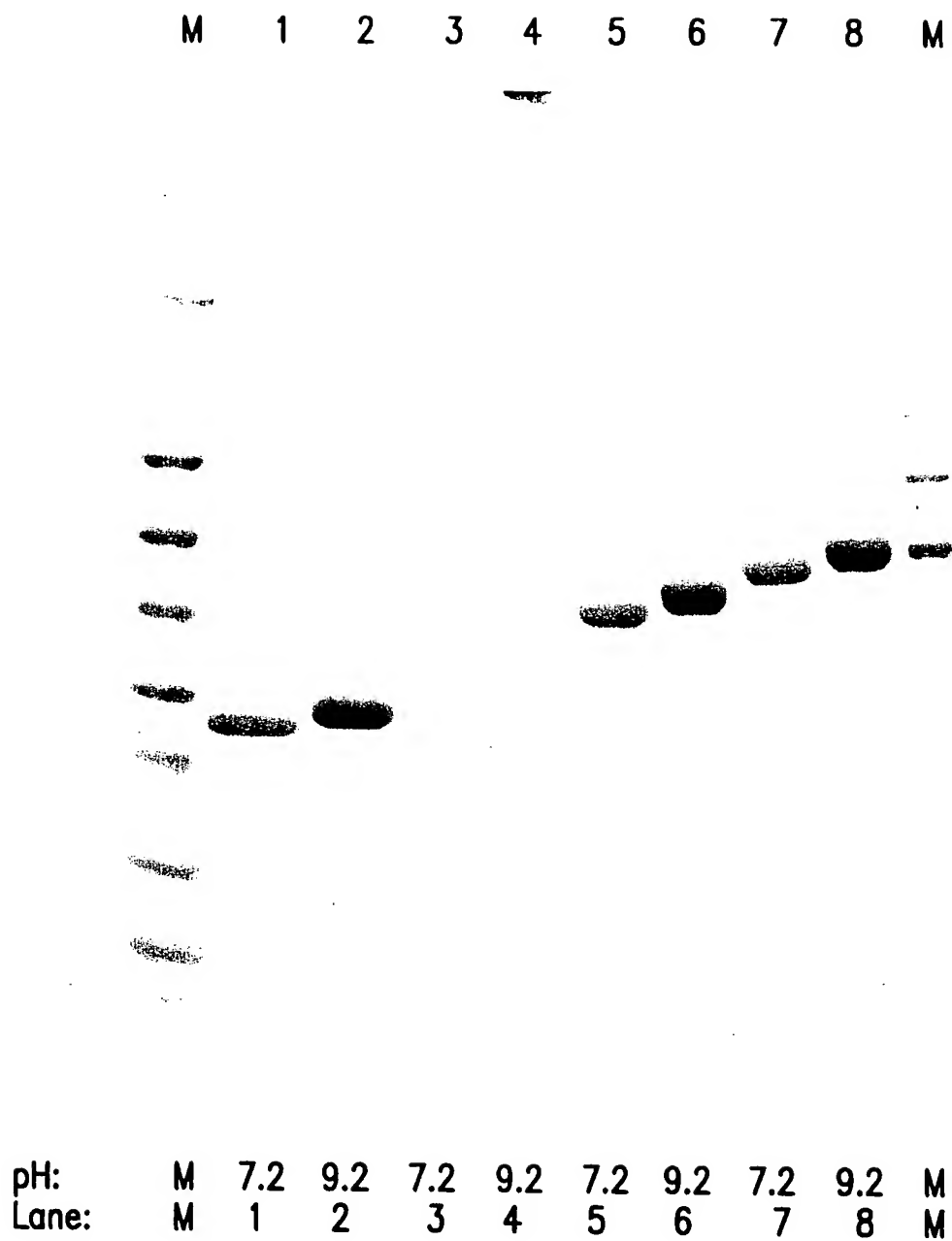


FIG.13